

## SEQUENCE LISTING

```
<110> Kimoto, Norihiro
        Yamamoto, Hiroaki
        Nakajima, Takanori
```

<120> Carbonyl reductases, polynucleotides comprising DNA encoding the same, methods for producing the same, and methods for producing optically active alcohol utilizing the same

<130> SHZ-021

<140>

<141>

<150> JP 2003-163015

<151> 2003-06-06

<150> JP 2003-113402

<151> 2003-04-17

<160> 25

<170> PatentIn version 3.1

<210> 1

<211> 1035

<212> DNA

<213> *Torulaspora delbrueckii*

**<220>**

<221> CDS

$\langle 222 \rangle$  (1) . . (1032)

<223>

<400> 1

atg tct att cta gtt tct ggt gct act ggt ttt att gct cta cat gtt 48  
Met Ser Ile Leu Val Ser Gly Ala Thr Gly Phe Ile Ala Leu His Val  
1 5 10 15

gtc agt gat ttg ttg aag cag gat tac aaa gtt att ggt act gtt aga 96  
Val Ser Asp Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr Val Arg  
20 25 30

tct caa gaa aaa gct gat aaa ttg cgt aag caa ttt ggc aac aat ccc      144  
Ser Gln Glu Lys Ala Asp Lys Leu Arg Lys Gln Phe Gly Asn Asn Pro  
          35                      40                      45

aat ctt tcc ttt gaa ttg gtt tca gat att gct gct cct gaa gct ttt 192  
Asn Leu Ser Phe Glu Leu Val Ser Asp Ile Ala Ala Pro Glu Ala Phe  
50 55 60

gac aaa gtc ttt cag aaa cat ggc aag gac atc aaa gtg gtg ttg cac 240  
Asp Lys Val Phe Gln Lys His Gly Lys Asp Ile Lys Val Val Leu His  
65 70 75 80

aca gct tct cct ttc act cta gaa acc aca aat tat gag aaa gat ctg	288
Thr Ala Ser Pro Phe Thr Leu Glu Thr Thr Asn Tyr Glu Lys Asp Leu	
85 90 95	
ttg ctt cca gca gtg aat ggt aca aag agt atc ctg gag tcg att aag	336
Leu Leu Pro Ala Val Asn Gly Thr Lys Ser Ile Leu Glu Ser Ile Lys	
100 105 110	
aaa tac gct gct gat tct gtc gag aga gta gtc atc aca tcg tct tac	384
Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Ile Thr Ser Ser Tyr	
115 120 125	
gct gcc gtc atg aat gtt tcg aaa gaa ggc gac ggc tca ata gtc tac	432
Ala Ala Val Met Asn Val Ser Lys Glu Gly Asp Gly Ser Ile Val Tyr	
130 135 140	
act gag aag gat tgg aac cct gcc act tgg gaa aac tgt cag ata gat	480
Thr Glu Lys Asp Trp Asn Pro Ala Thr Trp Glu Asn Cys Gln Ile Asp	
145 150 155 160	
ggt ttg aat gct tat tgt ggg tcc aag aag cta gca gaa aag gct gca	528
Gly Leu Asn Ala Tyr Cys Gly Ser Lys Lys Leu Ala Glu Lys Ala Ala	
165 170 175	
tgg gac ttc ttt gaa gat aat aaa aac gtt gtc aag ttc aaa ctg agc	576
Trp Asp Phe Phe Glu Asp Asn Lys Asn Val Val Lys Phe Lys Leu Ser	
180 185 190	
atg atc aat cct act tac gtt ttc ggg cct cag cta ttt gat gag gac	624
Met Ile Asn Pro Thr Tyr Val Phe Gly Pro Gln Leu Phe Asp Glu Asp	
195 200 205	
gtg aag gat aaa ttg aat act tcc tgt gag cta att aac tca att ata	672
Val Lys Asp Lys Leu Asn Thr Ser Cys Glu Leu Ile Asn Ser Ile Ile	
210 215 220	
aag aat aat cct cag gtg gga tat cta tta gag aat att aaa ggt cat	720
Lys Asn Asn Pro Gln Val Gly Tyr Leu Leu Glu Asn Ile Lys Gly His	
225 230 235 240	
ttc gtt gat gtc aga gat gtt gct aag gct cac ttg gtg gca ttc caa	768
Phe Val Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln	
245 250 255	
aag gat gaa gct att gga cag aga ctg ctc acc tca aat ggt cgt ttc	816
Lys Asp Glu Ala Ile Gly Gln Arg Leu Leu Thr Ser Asn Gly Arg Phe	
260 265 270	
gct tac caa gac ctc gta gat att atc aat gag gat ttc cca caa ttg	864
Ala Tyr Gln Asp Leu Val Asp Ile Ile Asn Glu Asp Phe Pro Gln Leu	
275 280 285	
aag ggt aag gtc att gta gga aag cca ggt gcc ggt aaa caa ttg tat	912
Lys Gly Lys Val Ile Val Gly Lys Pro Gly Ala Gly Lys Gln Leu Tyr	
290 295 300	

ggc act ttc cca gac atc aac aac acc aga tcg aag gag att ttg ggc 960  
 Gly Thr Phe Pro Asp Ile Asn Asn Thr Arg Ser Lys Glu Ile Leu Gly  
 305 310 315 320

ttc gaa ttc atc tct ctg cat aaa tcc gtc cat gac act gct gct caa 1008  
 Phe Glu Phe Ile Ser Leu His Lys Ser Val His Asp Thr Ala Ala Gln  
 325 330 335

gtt ttg aaa aaa gaa ggc aaa ttg taa 1035  
 Val Leu Lys Lys Glu Gly Lys Leu  
 340

<210> 2  
 <211> 344  
 <212> PRT  
 <213> *Torulaspora delbrueckii*

<400> 2  
 Met Ser Ile Leu Val Ser Gly Ala Thr Gly Phe Ile Ala Leu His Val  
 1 5 10 15

Val Ser Asp Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr Val Arg  
 20 25 30

Ser Gln Glu Lys Ala Asp Lys Leu Arg Lys Gln Phe Gly Asn Asn Pro  
 35 40 45

Asn Leu Ser Phe Glu Leu Val Ser Asp Ile Ala Ala Pro Glu Ala Phe  
 50 55 60

Asp Lys Val Phe Gln Lys His Gly Lys Asp Ile Lys Val Val Leu His  
 65 70 75 80

Thr Ala Ser Pro Phe Thr Leu Glu Thr Thr Asn Tyr Glu Lys Asp Leu  
 85 90 95

Leu Leu Pro Ala Val Asn Gly Thr Lys Ser Ile Leu Glu Ser Ile Lys  
 100 105 110

Lys Tyr Ala Ala Asp Ser Val Glu Arg Val Val Ile Thr Ser Ser Tyr  
 115 120 125

Ala Ala Val Met Asn Val Ser Lys Glu Gly Asp Gly Ser Ile Val Tyr  
 130 135 140

Thr Glu Lys Asp Trp Asn Pro Ala Thr Trp Glu Asn Cys Gln Ile Asp  
 145 150 155 160

Gly Leu Asn Ala Tyr Cys Gly Ser Lys Lys Leu Ala Glu Lys Ala Ala  
 165 170 175

Trp Asp Phe Phe Glu Asp Asn Lys Asn Val Val Lys Phe Lys Leu Ser  
 180 185 190

Met Ile Asn Pro Thr Tyr Val Phe Gly Pro Gln Leu Phe Asp Glu Asp  
 195 200 205  
 Val Lys Asp Lys Leu Asn Thr Ser Cys Glu Leu Ile Asn Ser Ile Ile  
 210 215 220  
 Lys Asn Asn Pro Gln Val Gly Tyr Leu Leu Glu Asn Ile Lys Gly His  
 225 230 235 240  
 Phe Val Asp Val Arg Asp Val Ala Lys Ala His Leu Val Ala Phe Gln  
 245 250 255  
 Lys Asp Glu Ala Ile Gly Gln Arg Leu Leu Thr Ser Asn Gly Arg Phe  
 260 265 270  
 Ala Tyr Gln Asp Leu Val Asp Ile Ile Asn Glu Asp Phe Pro Gln Leu  
 275 280 285  
 Lys Gly Lys Val Ile Val Gly Lys Pro Gly Ala Gly Lys Gln Leu Tyr  
 290 295 300  
 Gly Thr Phe Pro Asp Ile Asn Asn Thr Arg Ser Lys Glu Ile Leu Gly  
 305 310 315 320  
 Phe Glu Phe Ile Ser Leu His Lys Ser Val His Asp Thr Ala Ala Gln  
 325 330 335  
 Val Leu Lys Lys Glu Gly Lys Leu  
 340

<210> 3  
 <211> 10  
 <212> PRT  
 <213> *Torulaspora delbrueckii*

<400> 3

Ser Ile Leu Val Ser Gly Ala Thr Gly Phe  
 1 5 10

<210> 4  
 <211> 11  
 <212> PRT

<213> *Torulaspora delbrueckii*

<400> 4

Asp Leu Leu Leu Pro Ala Val Asn Gly Thr Lys  
 1 5 10

<210> 5  
 <211> 32  
 <212> DNA

<213> Artificial  
 <220>  
 <223> an artificially synthesized primer sequence  
 <220>  
 <221> misc\_feature  
 <222> (30)..(30)  
 <223> "n" = a, t, c, or g.  
 <400> 5  
 gtcgaattca tytttrgtbtc hggwgchacn gg 32  
 <210> 6  
 <211> 29  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> an artificially synthesized primer sequence  
 <220>  
 <221> misc\_feature  
 <222> (27)..(27)  
 <223> "n" = a, t, c, or g.  
 <400> 6  
 gtcgaattct tdgtwccrctt vacdgcngg 29  
 <210> 7  
 <211> 306  
 <212> DNA  
 <213> *Torulaspora delbrueckii*  
 <400> 7  
 attttagtgt ccggtgcaac aggtttttatt gctctacatg ttgtcagtga tttgttgaag 60  
 caggattaca aagttattgg tactgttaga tctcaagaaa aagctgataa attgctgaag 120  
 caatttggca acaatcccaa tctttccttt gaattgggtt cagatattgc tgctcctgaa 180  
 gcttttgaca aagtctttca gaaacatggc aaggacatca aagtgggtgtt gcacacagct 240  
 tctcctttca ctctagaaac caciaattat gagaaagatc tgttgcttcc tgccgtcaac 300  
 ggtact 306  
 <210> 8  
 <211> 30  
 <212> DNA  
 <213> Artificial  
 <220>  
 <223> an artificially synthesized primer sequence

<400> 8  
 ctaacagtac caataacttt gtaatcctgc 30

<210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 9  
 cacagcttct cctttcactc 20

<210> 10  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 10  
 gtcggatcct atcatgagta ttcttgtttc tgggtgctact gg 42

<210> 11  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 11  
 gtggtttcta gagtgaagc agaagc 26

<210> 12  
 <211> 36  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 12  
 ctttcactct agaaaccaca aattatgaga aagatc 36

<210> 13  
 <211> 53  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence  
  
 <400> 13  
 gacctgcagt atctagatta caatttgcct tctttttttca aaacttgagc agc 53  
  
 <210> 14  
 <211> 30  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> an artificially synthesized primer sequence  
  
 <400> 14  
 gagtcacgac tactgatacc actgttttcg 30  
  
 <210> 15  
 <211> 40  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> an artificially synthesized primer sequence  
  
 <400> 15  
 gagtctagat tatgcttcac tttgaacttc taacatttgc 40  
  
 <210> 16  
 <211> 1044  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*  
  
 <220>  
 <221> CDS  
 <222> (1)..(1041)  
 <223>  
  
 <400> 16  
 atg act act gat acc act gtt ttc gtt tct ggc gca acc ggt ttc att 48  
 Met Thr Thr Asp Thr Thr Val Phe Val Ser Gly Ala Thr Gly Phe Ile  
 1 5 10 15  
  
 gct cta cac att atg aac gat ctg ttg aaa gct ggc tat aca gtc atc 96  
 Ala Leu His Ile Met Asn Asp Leu Leu Lys Ala Gly Tyr Thr Val Ile  
 20 25 30  
  
 ggc tca ggt aga tct caa gaa aaa aat gat ggc ttg ctc aaa aaa ttt 144  
 Gly Ser Gly Arg Ser Gln Glu Lys Asn Asp Gly Leu Leu Lys Lys Phe  
 35 40 45  
  
 aat aac aat ccc aaa cta tcg atg gaa att gtg gaa gat att gct gct 192  
 Asn Asn Asn Pro Lys Leu Ser Met Glu Ile Val Glu Asp Ile Ala Ala

50	55	60	
cca aac gcc ttt gat gaa gtt ttc aaa aaa cat ggt aag gaa att aag Pro Asn Ala Phe Asp Glu Val Phe Lys Lys His Gly Lys Glu Ile Lys 65 70 75 80			240
att gtg cta cac act gcc tcc cca ttc cat ttt gaa act acc aat ttt Ile Val Leu His Thr Ala Ser Pro Phe His Phe Glu Thr Thr Asn Phe 85 90 95			288
gaa aag gat tta cta acc cct gca gtg aac ggt aca aaa tct atc ttg Glu Lys Asp Leu Leu Thr Pro Ala Val Asn Gly Thr Lys Ser Ile Leu 100 105 110			336
gaa gcg att aaa aaa tat gct gca gac act gtt gaa aaa gtt att gtt Glu Ala Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Lys Val Ile Val 115 120 125			384
act tcg tct act gct gct ctg gtg aca cct aca gac atg aac aaa gga Thr Ser Ser Thr Ala Ala Leu Val Thr Pro Thr Asp Met Asn Lys Gly 130 135 140			432
gat ttg gtg atc acg gag gag agt tgg aat aag gat aca tgg gac agt Asp Leu Val Ile Thr Glu Glu Ser Trp Asn Lys Asp Thr Trp Asp Ser 145 150 155 160			480
tgt caa gcc aac gcc gtt gcc gca tat tgt ggc tcg aaa aag ttt gct Cys Gln Ala Asn Ala Val Ala Ala Tyr Cys Gly Ser Lys Lys Phe Ala 165 170 175			528
gaa aaa act gct tgg gaa ttt ctt aaa gaa aac aag tct agt gtc aaa Glu Lys Thr Ala Trp Glu Phe Leu Lys Glu Asn Lys Ser Ser Val Lys 180 185 190			576
ttc aca cta tcc act atc aat ccg gga ttc gtt ttt ggt cct caa atg Phe Thr Leu Ser Thr Ile Asn Pro Gly Phe Val Phe Gly Pro Gln Met 195 200 205			624
ttt gca gat tcg cta aaa cat ggc ata aat acc tcc tca ggg atc gta Phe Ala Asp Ser Leu Lys His Gly Ile Asn Thr Ser Ser Gly Ile Val 210 215 220			672
tct gag tta att cat tcc aag gta ggt gga gaa ttt tat aat tac tgt Ser Glu Leu Ile His Ser Lys Val Gly Gly Glu Phe Tyr Asn Tyr Cys 225 230 235 240			720
ggc cca ttt att gac gtg cgt gac gtt tct aaa gcc cac cta gtt gca Gly Pro Phe Ile Asp Val Arg Asp Val Ser Lys Ala His Leu Val Ala 245 250 255			768
att gaa aaa cca gaa tgt acc ggc caa aga tta gta ttg agt gaa ggt Ile Glu Lys Pro Glu Cys Thr Gly Gln Arg Leu Val Leu Ser Glu Gly 260 265 270			816
tta ttc tgc tgt caa gaa atc gtt gac atc ttg aac gag gaa ttc cct			864



Leu Phe Cys Cys Gln Glu Ile Val Asp Ile Leu Asn Glu Glu Phe Pro  
 275 280 285  
 caa tta aag ggc aag ata gct aca ggt gaa cct gcg acc ggt cca agc 912  
 Gln Leu Lys Gly Lys Ile Ala Thr Gly Glu Pro Ala Thr Gly Pro Ser  
 290 295 300  
 ttt tta gaa aaa aac tct tgc aag ttt gac aat tct aag aca aaa aaa 960  
 Phe Leu Glu Lys Asn Ser Cys Lys Phe Asp Asn Ser Lys Thr Lys Lys  
 305 310 315 320  
 cta ctg gga ttc cag ttt tac aat tta aag gat tgc ata gtt gac acc 1008  
 Leu Leu Gly Phe Gln Phe Tyr Asn Leu Lys Asp Cys Ile Val Asp Thr  
 325 330 335  
 gcg gcg caa atg tta gaa gtt caa aat gaa gcc taa 1044  
 Ala Ala Gln Met Leu Glu Val Gln Asn Glu Ala  
 340 345

<210> 17  
 <211> 347  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 17  
 Met Thr Thr Asp Thr Thr Val Phe Val Ser Gly Ala Thr Gly Phe Ile  
 1 5 10 15  
 Ala Leu His Ile Met Asn Asp Leu Leu Lys Ala Gly Tyr Thr Val Ile  
 20 25 30  
 Gly Ser Gly Arg Ser Gln Glu Lys Asn Asp Gly Leu Leu Lys Lys Phe  
 35 40 45  
 Asn Asn Asn Pro Lys Leu Ser Met Glu Ile Val Glu Asp Ile Ala Ala  
 50 55 60  
 Pro Asn Ala Phe Asp Glu Val Phe Lys Lys His Gly Lys Glu Ile Lys  
 65 70 75 80  
 Ile Val Leu His Thr Ala Ser Pro Phe His Phe Glu Thr Thr Asn Phe  
 85 90 95  
 Glu Lys Asp Leu Leu Thr Pro Ala Val Asn Gly Thr Lys Ser Ile Leu  
 100 105 110  
 Glu Ala Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Lys Val Ile Val  
 115 120 125  
 Thr Ser Ser Thr Ala Ala Leu Val Thr Pro Thr Asp Met Asn Lys Gly  
 130 135 140  
 Asp Leu Val Ile Thr Glu Glu Ser Trp Asn Lys Asp Thr Trp Asp Ser  
 145 150 155 160

Cys Gln Ala Asn Ala Val Ala Ala Tyr Cys Gly Ser Lys Lys Phe Ala  
 165 170 175  
 Glu Lys Thr Ala Trp Glu Phe Leu Lys Glu Asn Lys Ser Ser Val Lys  
 180 185 190  
 Phe Thr Leu Ser Thr Ile Asn Pro Gly Phe Val Phe Gly Pro Gln Met  
 195 200 205  
 Phe Ala Asp Ser Leu Lys His Gly Ile Asn Thr Ser Ser Gly Ile Val  
 210 215 220  
 Ser Glu Leu Ile His Ser Lys Val Gly Gly Glu Phe Tyr Asn Tyr Cys  
 225 230 235 240  
 Gly Pro Phe Ile Asp Val Arg Asp Val Ser Lys Ala His Leu Val Ala  
 245 250 255  
 Ile Glu Lys Pro Glu Cys Thr Gly Gln Arg Leu Val Leu Ser Glu Gly  
 260 265 270  
 Leu Phe Cys Cys Gln Glu Ile Val Asp Ile Leu Asn Glu Glu Phe Pro  
 275 280 285  
 Gln Leu Lys Gly Lys Ile Ala Thr Gly Glu Pro Ala Thr Gly Pro Ser  
 290 295 300  
 Phe Leu Glu Lys Asn Ser Cys Lys Phe Asp Asn Ser Lys Thr Lys Lys  
 305 310 315 320  
 Leu Leu Gly Phe Gln Phe Tyr Asn Leu Lys Asp Cys Ile Val Asp Thr  
 325 330 335  
 Ala Ala Gln Met Leu Glu Val Gln Asn Glu Ala  
 340 345

<210> 18  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 18  
 cgagtcatga ctactgagaa aaccgttgtg tttgtttctg gtgc

44

<210> 19  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <223> an artificially synthesized primer sequence

<400> 19  
cgagctagca ttagctttta ctttgaactt ctagtaattg cgag 44

<210> 20  
<211> 1047  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1) .. (1044)  
<223>

<400> 20  
atg act act gaa aaa acc gtt gtt ttt gtt tct ggt gct act ggt ttc 48  
Met Thr Thr Glu Lys Thr Val Val Phe Val Ser Gly Ala Thr Gly Phe  
1 5 10 15

att gct cta cac gta gtg gac gat tta tta aaa act ggt tac aag gtc 96  
Ile Ala Leu His Val Val Asp Asp Leu Leu Lys Thr Gly Tyr Lys Val  
20 25 30

atc ggt tcg ggt agg tcc caa gaa aag aat gat gga ttg ctg aaa aaa 144  
Ile Gly Ser Gly Arg Ser Gln Glu Lys Asn Asp Gly Leu Leu Lys Lys  
35 40 45

ttt aag agc aat ccc aac ctt tca atg gag att gtc gaa gac att gct 192  
Phe Lys Ser Asn Pro Asn Leu Ser Met Glu Ile Val Glu Asp Ile Ala  
50 55 60

gct cca aac gct ttt gac aaa gtt ttt caa aag cac ggc aaa gag atc 240  
Ala Pro Asn Ala Phe Asp Lys Val Phe Gln Lys His Gly Lys Glu Ile  
65 70 75 80

aag gtt gtc ttg cac ata gct tct ccg gtt cac ttc aac acc act gat 288  
Lys Val Val Leu His Ile Ala Ser Pro Val His Phe Asn Thr Thr Asp  
85 90 95

ttc gaa aag gat ctg cta att cct gct gtg aat ggt acc aag tcc att 336  
Phe Glu Lys Asp Leu Leu Ile Pro Ala Val Asn Gly Thr Lys Ser Ile  
100 105 110

cta gaa gca atc aaa aat tat gcc gca gac aca gtc gaa aaa gtc gtt 384  
Leu Glu Ala Ile Lys Asn Tyr Ala Ala Asp Thr Val Glu Lys Val Val  
115 120 125

att act tct tct gtt gct gcc ctt gca tct ccc gga gat atg aag gac 432  
Ile Thr Ser Ser Val Ala Ala Leu Ala Ser Pro Gly Asp Met Lys Asp  
130 135 140

act agt ttc gtt gtc aat gag gaa agt tgg aac aaa gat act tgg gaa 480  
Thr Ser Phe Val Val Asn Glu Glu Ser Trp Asn Lys Asp Thr Trp Glu  
145 150 155 160

agt tgt caa gct aac gcg gtt tcc gca tac tgt ggt tcc aag aaa ttt 528  
Ser Cys Gln Ala Asn Ala Val Ser Ala Tyr Cys Gly Ser Lys Lys Phe

165										170					175					
gct gaa aaa act gct tgg gat ttt ctc gag gaa aac caa tca agc atc	576																			
Ala Glu Lys Thr Ala Trp Asp Phe Leu Glu Glu Asn Gln Ser Ser Ile																				
180 185 190																				
aaa ttt acg cta tca acc atc aac cca gga ttt gtt ttt ggc cct cag	624																			
Lys Phe Thr Leu Ser Thr Ile Asn Pro Gly Phe Val Phe Gly Pro Gln																				
195 200 205																				
cta ttt gcc gac tct ctt aga aat gga ata aat agc tct tca gcc att	672																			
Leu Phe Ala Asp Ser Leu Arg Asn Gly Ile Asn Ser Ser Ser Ala Ile																				
210 215 220																				
att gcc aat ttg gtt agt tat aaa tta ggc gac aat ttt tat aat tac	720																			
Ile Ala Asn Leu Val Ser Tyr Lys Leu Gly Asp Asn Phe Tyr Asn Tyr																				
225 230 235 240																				
agt ggt cct ttt att gac gtt cgc gat gtt tca aaa gct cat tta ctt	768																			
Ser Gly Pro Phe Ile Asp Val Arg Asp Val Ser Lys Ala His Leu Leu																				
245 250 255																				
gca ttt gag aaa ccc gaa tgc gct ggc caa aga cta ttc tta tgt gaa	816																			
Ala Phe Glu Lys Pro Glu Cys Ala Gly Gln Arg Leu Phe Leu Cys Glu																				
260 265 270																				
gat atg ttt tgc tct caa gaa gcg ctg gat atc ttg aat gag gaa ttt	864																			
Asp Met Phe Cys Ser Gln Glu Ala Leu Asp Ile Leu Asn Glu Glu Phe																				
275 280 285																				
cca cag tta aaa ggc aag ata gca act ggc gaa cct ggt agc ggc tca	912																			
Pro Gln Leu Lys Gly Lys Ile Ala Thr Gly Glu Pro Gly Ser Gly Ser																				
290 295 300																				
acc ttt ttg aca aaa aac tgc tgc aag tgc gac aac cgc aaa acc aaa	960																			
Thr Phe Leu Thr Lys Asn Cys Cys Lys Cys Asp Asn Arg Lys Thr Lys																				
305 310 315 320																				
aat tta tta gga ttc caa ttt aat aag ttc aga gat tgc att gtc gat	1008																			
Asn Leu Leu Gly Phe Gln Phe Asn Lys Phe Arg Asp Cys Ile Val Asp																				
325 330 335																				
act gcc tcg caa tta cta gaa gtt caa agt aaa agc taa	1047																			
Thr Ala Ser Gln Leu Leu Glu Val Gln Ser Lys Ser																				
340 345																				

<210> 21  
 <211> 348  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 21

Met Thr Thr Glu Lys Thr Val Val Phe Val Ser Gly Ala Thr Gly Phe
1 5 10 15

Ile Ala Leu His Val Val Asp Asp Leu Leu Lys Thr Gly Tyr Lys Val  
 20 25 30  
 Ile Gly Ser Gly Arg Ser Gln Glu Lys Asn Asp Gly Leu Leu Lys Lys  
 35 40 45  
 Phe Lys Ser Asn Pro Asn Leu Ser Met Glu Ile Val Glu Asp Ile Ala  
 50 55 60  
 Ala Pro Asn Ala Phe Asp Lys Val Phe Gln Lys His Gly Lys Glu Ile  
 65 70 75 80  
 Lys Val Val Leu His Ile Ala Ser Pro Val His Phe Asn Thr Thr Asp  
 85 90 95  
 Phe Glu Lys Asp Leu Leu Ile Pro Ala Val Asn Gly Thr Lys Ser Ile  
 100 105 110  
 Leu Glu Ala Ile Lys Asn Tyr Ala Ala Asp Thr Val Glu Lys Val Val  
 115 120 125  
 Ile Thr Ser Ser Val Ala Ala Leu Ala Ser Pro Gly Asp Met Lys Asp  
 130 135 140  
 Thr Ser Phe Val Val Asn Glu Glu Ser Trp Asn Lys Asp Thr Trp Glu  
 145 150 155 160  
 Ser Cys Gln Ala Asn Ala Val Ser Ala Tyr Cys Gly Ser Lys Lys Phe  
 165 170 175  
 Ala Glu Lys Thr Ala Trp Asp Phe Leu Glu Glu Asn Gln Ser Ser Ile  
 180 185 190  
 Lys Phe Thr Leu Ser Thr Ile Asn Pro Gly Phe Val Phe Gly Pro Gln  
 195 200 205  
 Leu Phe Ala Asp Ser Leu Arg Asn Gly Ile Asn Ser Ser Ser Ala Ile  
 210 215 220  
 Ile Ala Asn Leu Val Ser Tyr Lys Leu Gly Asp Asn Phe Tyr Asn Tyr  
 225 230 235 240  
 Ser Gly Pro Phe Ile Asp Val Arg Asp Val Ser Lys Ala His Leu Leu  
 245 250 255  
 Ala Phe Glu Lys Pro Glu Cys Ala Gly Gln Arg Leu Phe Leu Cys Glu  
 260 265 270  
 Asp Met Phe Cys Ser Gln Glu Ala Leu Asp Ile Leu Asn Glu Glu Phe  
 275 280 285  
 Pro Gln Leu Lys Gly Lys Ile Ala Thr Gly Glu Pro Gly Ser Gly Ser  
 290 295 300  
 Thr Phe Leu Thr Lys Asn Cys Cys Lys Cys Asp Asn Arg Lys Thr Lys  
 305 310 315 320

Asn Leu Leu Gly Phe Gln Phe Asn Lys Phe Arg Asp Cys Ile Val Asp  
325 330 335

Thr Ala Ser Gln Leu Leu Glu Val Gln Ser Lys Ser  
340 345

<210> 22  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> an artificially synthesized primer sequence

<400> 22  
gcaacatgct taatacagtt ctagtttctg 30

<210> 23  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<223> an artificially synthesized primer sequence

<400> 23  
ggttctagat tataaacggt tctccttctt caaaatttgg g 41

<210> 24  
<211> 1035  
<212> DNA  
<213> *Saccharomyces cerevisiae*

<220>  
<221> CDS  
<222> (1)..(1032)  
<223>

<400> 24  
atg tct aat aca gtt cta gtt tct ggc gct tca ggt ttt att gcc ttg 48  
Met Ser Asn Thr Val Leu Val Ser Gly Ala Ser Gly Phe Ile Ala Leu  
1 5 10 15

cat atc ctg tca caa ttg tta aaa caa gat tat aag gtt att gga act 96  
His Ile Leu Ser Gln Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr  
20 25 30

gtg aga tcc cat gaa aaa gaa gca aaa ttg cta aga caa ttt caa cat 144  
Val Arg Ser His Glu Lys Glu Ala Lys Leu Leu Arg Gln Phe Gln His  
35 40 45

aac cct aat tta act tta gaa att gtt ccg gac att tct cat cca aat 192  
Asn Pro Asn Leu Thr Leu Glu Ile Val Pro Asp Ile Ser His Pro Asn

50	55	60	
gct ttc gat aag gtt ctg cag aaa cgt gga cgt gag att agg tat gtt Ala Phe Asp Lys Val Leu Gln Lys Arg Gly Arg Glu Ile Arg Tyr Val 65 70 75 80			240
cta cac acg gcc tct cct ttt cat tat gat act acc gaa tat gaa aaa Leu His Thr Ala Ser Pro Phe His Tyr Asp Thr Thr Glu Tyr Glu Lys 85 90 95			288
gac tta ttg att ccc gcg tta gaa ggt aca aaa aac atc cta aat tct Asp Leu Leu Ile Pro Ala Leu Glu Gly Thr Lys Asn Ile Leu Asn Ser 100 105 110			336
atc aag aaa tat gca gca gac act gta gag cgt gtt gtt gtg act tct Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Arg Val Val Val Thr Ser 115 120 125			384
tct tgt act gct att ata acc ctt gca aag atg gac gat ccc agt gtg Ser Cys Thr Ala Ile Ile Thr Leu Ala Lys Met Asp Asp Pro Ser Val 130 135 140			432
gtt ttt aca gaa gag agt tgg aac gaa gca acc tgg gaa agc tgt caa Val Phe Thr Glu Glu Ser Trp Asn Glu Ala Thr Trp Glu Ser Cys Gln 145 150 155 160			480
att gat ggg ata aat gct tac ttt gca tcc aag aag ttt gct gaa aag Ile Asp Gly Ile Asn Ala Tyr Phe Ala Ser Lys Lys Phe Ala Glu Lys 165 170 175			528
gct gcc tgg gag ttc aca aaa gag aat gaa gat cac atc aaa ttc aaa Ala Ala Trp Glu Phe Thr Lys Glu Asn Glu Asp His Ile Lys Phe Lys 180 185 190			576
cta aca aca gtc aac cct tct ctt ctt ttt ggt cct caa ctt ttc gat Leu Thr Thr Val Asn Pro Ser Leu Leu Phe Gly Pro Gln Leu Phe Asp 195 200 205			624
gaa gat gtg cat ggc cat ttg aat act tct tgc gaa atg atc aat ggc Glu Asp Val His Gly His Leu Asn Thr Ser Cys Glu Met Ile Asn Gly 210 215 220			672
cta att cat acc cca gta aat gcc agt gtt cct gat ttt cat tcc att Leu Ile His Thr Pro Val Asn Ala Ser Val Pro Asp Phe His Ser Ile 225 230 235 240			720
ttt att gat gta agg gat gtg gcc cta gct cat ctg tat gct ttc cag Phe Ile Asp Val Arg Asp Val Ala Leu Ala His Leu Tyr Ala Phe Gln 245 250 255			768
aag gaa aat acc gcg ggt aaa aga tta gtg gta act aac ggt aaa ttt Lys Glu Asn Thr Ala Gly Lys Arg Leu Val Val Thr Asn Gly Lys Phe 260 265 270			816
gga aac caa gat atc ctg gat att ttg aac gaa gat ttt cca caa tta Gly Asn Gln Asp Ile Leu Asp Ile Leu Asn Glu Asp Phe Pro Gln Leu 275 280 285			864

aga ggt ctc att cct ttg ggt aag cct ggc aca ggt gat caa gtc att 912  
 Arg Gly Leu Ile Pro Leu Gly Lys Pro Gly Thr Gly Asp Gln Val Ile  
 290 295 300

gac cgc ggt tca act aca gat aat agt gca acg agg aaa ata ctt ggc 960  
 Asp Arg Gly Ser Thr Thr Asp Asn Ser Ala Thr Arg Lys Ile Leu Gly  
 305 310 315 320

ttt gag ttc aga agt tta cac gaa agt gtc cat gat act gct gcc caa 1008  
 Phe Glu Phe Arg Ser Leu His Glu Ser Val His Asp Thr Ala Ala Gln  
 325 330 335

att ttg aag aag gag aac aga tta tga 1035  
 Ile Leu Lys Lys Glu Asn Arg Leu  
 340

<210> 25  
 <211> 344  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 25

Met Ser Asn Thr Val Leu Val Ser Gly Ala Ser Gly Phe Ile Ala Leu  
 1 5 10 15

His Ile Leu Ser Gln Leu Leu Lys Gln Asp Tyr Lys Val Ile Gly Thr  
 20 25 30

Val Arg Ser His Glu Lys Glu Ala Lys Leu Leu Arg Gln Phe Gln His  
 35 40 45

Asn Pro Asn Leu Thr Leu Glu Ile Val Pro Asp Ile Ser His Pro Asn  
 50 55 60

Ala Phe Asp Lys Val Leu Gln Lys Arg Gly Arg Glu Ile Arg Tyr Val  
 65 70 75 80

Leu His Thr Ala Ser Pro Phe His Tyr Asp Thr Thr Glu Tyr Glu Lys  
 85 90 95

Asp Leu Leu Ile Pro Ala Leu Glu Gly Thr Lys Asn Ile Leu Asn Ser  
 100 105 110

Ile Lys Lys Tyr Ala Ala Asp Thr Val Glu Arg Val Val Val Thr Ser  
 115 120 125

Ser Cys Thr Ala Ile Ile Thr Leu Ala Lys Met Asp Asp Pro Ser Val  
 130 135 140

Val Phe Thr Glu Glu Ser Trp Asn Glu Ala Thr Trp Glu Ser Cys Gln  
 145 150 155 160

Ile Asp Gly Ile Asn Ala Tyr Phe Ala Ser Lys Lys Phe Ala Glu Lys  
 165 170 175



Ala	Ala	Trp	Glu	Phe	Thr	Lys	Glu	Asn	Glu	Asp	His	Ile	Lys	Phe	Lys	180	185	190
Leu	Thr	Thr	Val	Asn	Pro	Ser	Leu	Leu	Phe	Gly	Pro	Gln	Leu	Phe	Asp	195	200	205
Glu	Asp	Val	His	Gly	His	Leu	Asn	Thr	Ser	Cys	Glu	Met	Ile	Asn	Gly	210	215	220
Leu	Ile	His	Thr	Pro	Val	Asn	Ala	Ser	Val	Pro	Asp	Phe	His	Ser	Ile	225	230	235
Phe	Ile	Asp	Val	Arg	Asp	Val	Ala	Leu	Ala	His	Leu	Tyr	Ala	Phe	Gln	245	250	255
Lys	Glu	Asn	Thr	Ala	Gly	Lys	Arg	Leu	Val	Val	Thr	Asn	Gly	Lys	Phe	260	265	270
Gly	Asn	Gln	Asp	Ile	Leu	Asp	Ile	Leu	Asn	Glu	Asp	Phe	Pro	Gln	Leu	275	280	285
Arg	Gly	Leu	Ile	Pro	Leu	Gly	Lys	Pro	Gly	Thr	Gly	Asp	Gln	Val	Ile	290	295	300
Asp	Arg	Gly	Ser	Thr	Thr	Asp	Asn	Ser	Ala	Thr	Arg	Lys	Ile	Leu	Gly	305	310	315
Phe	Glu	Phe	Arg	Ser	Leu	His	Glu	Ser	Val	His	Asp	Thr	Ala	Ala	Gln	325	330	335
Ile	Leu	Lys	Lys	Glu	Asn	Arg	Leu									340		